

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 1, 2001, 15:47:07 ; Search time 210.42 Seconds
(without alignments)
7.313 Million cell updates/sec

Title: US-09-331-631a-3_COPY_29_73

Perfect score: 252
Sequence: 1 SEFPROXEYECCKROCMOLET.....RCVSQCDKFEEDIDWSKYD 45

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 268485 segs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_36:*

- 1: /SIDSI/gcgdata/geneseq/geneseqp/AA1980.DAT.*
- 2: /SIDSI/gcgdata/geneseq/geneseqp/AA1981.DAT.*
- 3: /SIDSI/gcgdata/geneseq/geneseqp/AA1982.DAT.*
- 4: /SIDSI/gcgdata/geneseq/geneseqp/AA1983.DAT.*
- 5: /SIDSI/gcgdata/geneseq/geneseqp/AA1984.DAT.*
- 6: /SIDSI/gcgdata/geneseq/geneseqp/AA1985.DAT.*
- 7: /SIDSI/gcgdata/geneseq/geneseqp/AA1986.DAT.*
- 8: /SIDSI/gcgdata/geneseq/geneseqp/AA1987.DAT.*
- 9: /SIDSI/gcgdata/geneseq/geneseqp/AA1988.DAT.*
- 10: /SIDSI/gcgdata/geneseq/geneseqp/AA1989.DAT.*
- 11: /SIDSI/gcgdata/geneseq/geneseqp/AA1990.DAT.*
- 12: /SIDSI/gcgdata/geneseq/geneseqp/AA1991.DAT.*
- 13: /SIDSI/gcgdata/geneseq/geneseqp/AA1992.DAT.*
- 14: /SIDSI/gcgdata/geneseq/geneseqp/AA1993.DAT.*
- 15: /SIDSI/gcgdata/geneseq/geneseqp/AA1994.DAT.*
- 16: /SIDSI/gcgdata/geneseq/geneseqp/AA1995.DAT.*
- 17: /SIDSI/gcgdata/geneseq/geneseqp/AA1996.DAT.*
- 18: /SIDSI/gcgdata/geneseq/geneseqp/AA1997.DAT.*
- 19: /SIDSI/gcgdata/geneseq/geneseqp/AA1998.DAT.*
- 20: /SIDSI/gcgdata/geneseq/geneseqp/AA1999.DAT.*
- 21: /SIDSI/gcgdata/geneseq/geneseqp/AA2000.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	252	100.0	666	19 W62828	Macadamia integrif
2	252	100.0	666	19 W62829	Macadamia integrif
3	180	71.4	625	19 W62830	Macadamia integrif
4	78.5	31.2	590	19 W62832	Gossypium hirsutum
5	70.5	28.0	525	19 W62831	Theobroma cacao an
6	70.5	28.0	566	13 R20181	Sequence encoded b
7	67	26.6	218	19 W40287	Human TSP1 protein
8	67	26.6	218	20 Y06182	Thrombospondin I f
9	67	26.6	239	14 R40823	Human thrombospond
10	67	26.6	441	19 W40288	Human concatametic
11	67	26.6	441	20 Y06183	Thrombospondin I f
12	63	25.0	444	20 W90340	G. max truncated S

13	63	25.0	524	20 W90339	G. max SBP1 protei
14	62.5	24.8	409	20 W90342	G. max truncated S
15	62.5	24.8	489	20 W90341	G. max SBP2 protei
16	62	24.6	941	21 V66736	Membrane-bound pro
17	59.5	23.6	2703	16 R70236	P. falciparum Proj
18	59.5	23.6	2710	18 W22482	P. falciparum Proj
19	59.5	23.6	2710	21 V77904	P. falciparum Proj
20	59.5	23.6	3060	18 W22475	Plasmodium var-7.
21	59.5	23.6	3060	21 V77905	Plasmodium var-7 p
22	57	22.6	1284	9 P81187	Sequence encoded b
23	56.5	22.4	593	19 W62835	Zea mays antimicro
24	55	21.8	623	20 W30622	Arabidopsis enhanc
25	55	21.8	816	16 R85870	WD-40 domain-contg
26	53.5	21.2	450	19 W56779	Human beclin prote
27	53.5	21.2	450	19 W56784	Human beclin prote
28	53	21.0	35	13 R21079	Antimicrobial maiz
29	52.5	20.8	569	20 V24054	Zea mays antimicro
30	52.5	20.8	569	21 Y83041	A human beta-trans
31	52.5	20.8	569	21 Y83250	F-box protein hbet
32	52.5	20.8	569	21 V44249	Human cell signal
33	52	20.6	33	19 W62836	Zea mays antimicro
34	52	20.6	58	20 V32115	Maize Id gene Nsl1
35	52	20.6	436	20 V32114	Maize Id protein.
36	52	20.6	623	20 W30620	Arabidopsis La-er
37	52	20.6	623	20 W30624	Arabidopsis mutant
38	51.5	20.4	147	13 R22950	Leech antiplatelet
39	51.5	20.4	569	21 Y83254	F-box protein FMD1
40	51.5	20.4	5250	21 V53678	Sequence gi/442661
41	49.5	19.6	98	17 R81709	AcanaP6. Ancylost
42	49.5	19.6	98	20 Y30395	Nematode extracted
43	49.5	19.6	562	18 W12096	Adenovirus E1A ass
44	49	19.4	411	21 V77914	Plasmodium DBL gen
45	49	19.4	467	21 V70814	Extended human zsi

ALIGNMENTS

RESULT 1	
ID	W62828 standard; Protein: 666 AA.
XX	
AC	W62828:
XX	
DT	27-OCT-1998 (first entry)
XX	
DE	Macadamia integrifolia antimicrobial protein.
XX	
KW	antimicrobial protein; Infestation; control.
OS	Macadamia integrifolia.
XX	
FT	Key
FT	Peptide
FT	Location/Qualifiers
FT	1..28
FT	/note= "signal peptide"
FT	29..666
FT	/note= "mature protein"
XX	
PN	W09827805-A1.
XX	
PD	02-JUL-1998.
XX	
PF	22-DEC-1997; 97WO-AU00874.
XX	
PR	20-DEC-1996; 96AU-0004275.
XX	
PA	(RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
XX	
PI	Bower NL, Goulter KC, Green JL, Manners JM, Marcus JP;
XX	
DR	WPI: 1998-377279/32.
XX	
DR	N-PSDB: V42310.
XX	

PT Novel anti-microbial protein from e.g. Macadamia integrifolia -
PT useful for controlling microbial infestations of plants or mammals
XX
PS Claim 1: Page 34-36; 96pp; English.
XX
CC The sequence is that of an antimicrobial protein which can
CC be used to control microbial infestations in plants and mammalian
CC animals.
XX
SQ Sequence 666 AA:

Query Match 100.0%; Score 252; DB 19; Length 666;
Best Local Similarity 100.0%; Pred. No. 2.3e-23;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SEFDROEYEECKRCQMQLTSGOMRRVCSQCDKRFEDIDWSKYD 45
Db 29 sefdroyeeckrcqmqltsgmrrvcsgcdkrfeedidwskyd 73

RESULT 2
W62829 standard; Protein: 666 AA.
AC W62829;
XX
DT 27-OCT-1998 (first entry)
XX
DE Macadamia integrifolia antimicrobial protein.
XX
KM antimicrobial protein; infestation; control.
OS Macadamia integrifolia.
XX
PI Bower NI, Goulter KC, Green JL, Manners JM, Marcus JP;
XX WPI: 1998-377279/32.
DR N-PSDB; VA2311.
XX
PT Novel anti-microbial protein from e.g. Macadamia integrifolia -
PT useful for controlling microbial infestations of plants or mammals
XX
PS Claim 1: Page 39-41; 96pp; English.
XX
CC The sequence is that of an antimicrobial protein which can
CC be used to control microbial infestations in plants and mammalian
CC animals.
XX
SQ Sequence 666 AA:

Query Match 100.0%; Score 252; DB 19; Length 666;
Best Local Similarity 100.0%; Pred. No. 2.3e-23;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SEFDROEYEECKRCQMQLTSGOMRRVCSQCDKRFEDIDWSKYD 45

Db 29 sefdroyeeckrcqmqltsgmrrvcsgcdkrfeedidwskyd 73

RESULT 3
W62830 standard; Protein: 625 AA.
XX
AC W62830;
XX
DT 27-OCT-1998 (first entry)
XX
DE Macadamia integrifolia antimicrobial protein.
XX
KM antimicrobial protein; infestation; control.
OS Macadamia integrifolia.
XX
PI Bower NI, Goulter KC, Green JL, Manners JM, Marcus JP;
XX WPI: 1998-377279/32.
DR N-PSDB; VA2316.
XX
PT Novel anti-microbial protein from e.g. Macadamia integrifolia -
PT useful for controlling microbial infestations of plants or mammals
XX
PS Claim 1: Page 43-45; 96pp; English.
XX
CC The sequence is that of an antimicrobial protein which can
CC be used to control microbial infestations in plants and mammalian
CC animals.
XX
SQ Sequence 625 AA:

Query Match 71.4%; Score 180; DB 19; Length 625;
Best Local Similarity 100.0%; Pred. No. 1.7e-14;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 QCMQLTSGOMRRVCSQCDKRFEDIDWSKYD 45
Db 1 qcmqltsgmrrvcsgcdkrfeedidwskyd 32

RESULT 4
W62832 standard; Protein: 590 AA.
XX
AC W62832;
XX
DT 27-OCT-1998 (first entry)
XX
DE Gossypium hirsutum antimicrobial protein.
XX
KM antimicrobial protein; infestation; control.
OS Gossypium hirsutum.

XX WO9827805-A1.
 PN 02-JUL-1998.
 PD 22-DEC-1997; 97WO-AU00874.
 XX PF 20-DEC-1996; 96AU-0004275.
 XX PR (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
 XX PI Bower NI, Goulter KC, Green JL, Manners JM, Marcus JP;
 XX WPI: 1998-377279/32.
 DR
 XX Novel anti-microbial protein from e.g. Macadamia integrifolia -
 PT useful for controlling microbial infestations of plants or mammals
 XX
 PS Claim 1; Page 49-51; 96pp; English.
 CC The sequence is that of an antimicrobial protein which can
 CC be used to control microbial infestations in plants and mammalian
 CC animals.
 CC
 SQ Sequence 590 AA;

Query Match 31.2%; Score 78.5; DB 19; Length 590;
 Best Local Similarity 40.5%; Pred. No. 0.055;
 Matches 15; Conservative 9; Mismatches 12; Indels 1; Gaps 1;
 QY 2 EPDRQYECKRQCMQLETSGQMRGVSCQDKRFEED 38
 Db 81 edpgrryecqgecqrge-erqgpcqqrclkrfege 116

RESULT 5
 ID W62831 standard; Protein: 525 AA.
 XX W62831;
 AC 27-OCT-1998 (first entry)
 DT Theobroma cacao antimicrobial protein.
 XX
 DE antimicrobial protein; infestation; control.
 XX
 KW Theobroma cacao.
 OS WO9827805-A1.
 XX
 PN 02-JUL-1998.
 PD 22-DEC-1997; 97WO-AU00874.
 XX PF 20-DEC-1996; 96AU-0004275.
 XX PR (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
 XX PI Bower NI, Goulter KC, Green JL, Manners JM, Marcus JP;
 XX WPI: 1998-377279/32.
 DR
 XX Novel anti-microbial protein from e.g. Macadamia integrifolia -
 PT useful for controlling microbial infestations of plants or mammals
 XX
 PS Claim 1; Page 47-49; 96pp; English.
 CC The sequence is that of an antimicrobial protein which can
 CC be used to control microbial infestations in plants and mammalian
 CC animals.
 CC

SQ Sequence 525 AA;
 Query Match 28.0%; Score 70.5; DB 19; Length 525;
 Best Local Similarity 32.4%; Pred. No. 0.47;
 Matches 11; Conservative 11; Mismatches 11; Indels 1; Gaps 1;
 QY 5 ROYEYECCKRQCMQLETSGQMRGVSCQDKRFEED 37
 Db 39 rqqyegqqrceateeregeqecqrcereyke 72

RESULT 6
 ID R20181 standard; Protein: 566 AA.
 XX R20181;
 AC 16-APR-1992 (first entry)
 DT Sequence encoded by 67 kD T. cacao protein cDNA.
 XX
 DE Cocoa; flavour; vicillin; seed storage protein.
 XX
 KW Theobroma cacao.
 OS WO9119801-A.
 XX
 PN 26-DEC-1991.
 PD 07-JUN-1991; 91WO-GB00914.
 XX PF 11-JUN-1990; 90GB-0013016.
 XX PR (MRS) MARS UK LTD.
 PA Spencer ME, Hodge R, Deakin EA, Ashton S;
 XX WPI: 1992-024418/03.
 DR N-PSDB; Q20377.
 DR
 XX Recombinant cocoa proteins - are responsible for flavour in cocoa
 PT beans and produced in large quantities using yeast and bacterial
 PT expression vectors
 PT
 PS Claim 4; Fig 2; 59pp; English.
 XX
 CC The inventors claim a 67 kD and 31 kD T. cacao protein, and
 CC fragments, and encoding DNAs. The 47 kD and 31 kD proteins are
 CC derived from the 67 kD precursor. T. cacao protein cDNA was
 CC detected in a cDNA library prepared from immature cocoa beans RNA.
 CC using a probe based on the AA sequence of a CNR peptide common to
 CC the 47 kD and 31 kD polypeptides. Homology searches revealed close
 CC homologues between the 67 kD polypeptide and the vicillins, which are
 CC seed storage proteins.
 CC
 SQ Sequence 566 AA;

Query Match 28.0%; Score 70.5; DB 13; Length 566;
 Best Local Similarity 32.4%; Pred. No. 0.51;
 Matches 11; Conservative 11; Mismatches 11; Indels 1; Gaps 1;
 QY 5 ROYEYECCKRQCMQLETSGQMRGVSCQDKRFEED 37
 Db 39 rqqyegqqrceateeregeqecqrcereyke 72
 RESULT 7
 ID W40287 standard; Protein: 218 AA.
 XX W40287;
 AC

[illegible]

KW		Thrombospondin I; melanoma; lung cancer; colon cancer;
KW		brain cancer; breast cancer.
XX		
OS	Homo sapiens.	
FH	Key	Location/Qualifiers
FT	Misc-difference 160	/note= "encoded by CCG"
FT	Misc-difference 161	/note= "encoded by CTC"
FT	Misc-difference 162	/note= "encoded by TGC"
FT	Misc-difference 163	/note= "encoded by AAC"
FT	Misc-difference 177	/note= "encoded by GAA"
FT	Misc-difference 178	/note= "encoded by GCG"
FT	Misc-difference 179	/note= "encoded by CCG"
XX		
PN	EP921193-A1.	
PD	09-JUN-1999.	
XX		
PF	07-JAN-1998;	98EP-0100135.
XX		
PR	05-DEC-1997;	97US-0985526.
XX		
PA	(MIXS/) MIXSON A J.	
XX		
PI	Mixson AJ;	
DR	WPI: 1999-315406/27.	
DR	N-PSDB; X58725.	
XX		
PRT	Inhibition of growth of solid tumors	
XX		
PS	Disclosure; Page 17-18; 46pp; English.	
XX		
CC	This sequence represents an anti-angiogenic fragment of the	
CC	thrombospondin I protein. The invention provides a carrier DNA	
CC	complex that comprises DNA (see X58725-42) coding for an	
CC	anti-angiogenic protein or peptide, and which additionally comprises	
CC	to the site of a tumour in vivo, and which additionally comprises	
CC	regulatory elements for expressing the anti-angiogenic DNA in a	
CC	tumour or tumour vasculature. The complex may also include DNA	
CC	encoding a tumour suppressor protein, especially p53. The carrier	
CC	is a liposome, cationic polymer, micelle, microsphere, virus, viral	
CC	component, or a combination of these, and administration is by	
CC	intravenous or intratumoral injection. The complexes are useful in	
CC	gene therapy for inhibition of tumour growth. The types of tumors	
CC	which may be treated include solid tumors such as melanomas and	
CC	tumors in the lung, colon, brain and breast.	
XX		
SQ	Sequence 218 AA:	
	Query Match 26.6%; Score 67; DB 20; Length 218;	
	Best Local Similarity 39.5%; Pred. No. 0.49;	
	Matches 15; Conservative 6; Mismatches 11; Indels 6; Gaps 2;	
OY	13 RCGMOLE-----TSGOMRRC-VSCDDKREEDIDMSKY 44	
	: : ::: :	
Db	104 rscdslmrcegssvqlrtchigecckrikqdgawshw 141	
RESULT 9		
R40823		
ID	R40823 standard; protein; 239 AA.	
XX		
AC	R40823;	
XX		

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DT 03-MAR-1994 (first entry)
XX
DE Human thrombospondin 1.
XX
KW hTSP-1: platelet glycoprotein; angiogenesis; neovascularisation;
KW inhibitor; solid tumour; skin cancer; angiogenic dysfunction;
KW melanoma; diabetic retinopathy; psoriasis; neovascular glaucoma;
KW Kaposi's sarcoma; inflammation; retrolental fibroplasia.
XX
OS Homo sapiens.
XX
PN MO9316716-A.
XX
PD 02-SEP-1993.
XX
PF 22-FEB-1993; 93WO-US01652.
XX
PR 24-FEB-1992; 92US-0841656.
XX
PA (NOUN ) UNIV NORTHWESTERN.
XX
PI Bouck NP, Frazier WA, Good DJ, Polverini PJ;
XX
DR WPT; 1993-288118/36.
XX
PT Compns. for inhibiting angiogenesis - conty. a vascularisation
PT inhibitor comprising a peptide capable of inhibiting
PT vascularisation
XX
PS Claim 10; Page 41-42; 51pp; English.
XX
CC Certain fragments of thrombospondin, a glycoprotein found in the
CC alpha granules of platelets, can inhibit vascularisation. Peptides
CC derived from the hTSP sequence are useful for inhibiting
CC neovascularisation, esp. in solid tumours such as melanomas. The
CC inhibitory peptides can also be used in other diseases involving
CC angiogenic dysfunction. See R40824-R40830.
CC
XX
SQ Sequence 239 AA;

Query Match 26.6%; Score 67; DB 14; Length 239;
Best Local Similarity 39.5%; Pred. No. 0.54;
Matches 15; Conservative 6; Mismatches 11; Indels 6; Gaps 2;

QY 13 ROCMOLE-----TSGOMRRC-VSQCCKRFEEDIDMSKY 44
| | | | | : : : : : | | | | | : : : : : | | |
Db 93 rscdslnrcegsvqtrchigcdkrtkqdgyswh 130

RESULT 10
W40288
ID W40288 standard; Protein: 441 AA.
XX
AC W40288;
XX
DT 18-AUG-1998 (first entry)
XX
DE Human concatamerised TSP1 protein.
XX
KW TSP1; thrombospondin; anti-angiogenic; cationic vehicle; gene therapy;
KW liposome; DNA complex; tumour suppressor protein; treatment; neoplastic;
KW metabolic disease; concatamer; tumour.
XX
OS Homo sapiens.
XX
XX
XX Key Location/Qualifiers
FH Misc-difference 160 /note= "encoded by CGG"
FT Misc-difference 221 /note= "encoded by GAC"
FT Misc-difference 383

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FT /note= "encoded by CGG"
FT Region 223..227
FT /label= intervening sequence
XX
PN EP819758-A2.
XX
PD 21-JAN-1998.
XX
PF 16-JUL-1997; 97EP-0112154.
XX
PR 16-JUL-1996; 96US-0680845.
XX
PA (MIXS/) MIXSON A J.
XX
PI Mixson AJ;
XX
DR WPT; 1998-078839/08.
XX
DR N-PSDB; V10494.
XX
PT Complexes of DNA encoding anti-angiogenic peptide - with cationic
PT liposome(s) or cationic polymer, useful for, e.g. gene therapy of
PT tumours
XX
PS Claim 9; Page 6-7; 47pp; English.
XX
CC This protein sequence represents a concatamer of thrombospondin TSP1
CC which is used in a method to produce a cationic vehicle consisting
CC of a cationic liposome:DNA complex where the DNA encodes an
CC anti-angiogenic peptide or tumour suppressor protein. Such complexes are
CC used for treatment of neoplastic and metabolic diseases especially for
CC gene therapy of tumours.
CC
XX
SQ Sequence 441 AA;

Query Match 26.6%; Score 67; DB 19; Length 441;
Best Local Similarity 39.5%; Pred. No. 1;
Matches 15; Conservative 6; Mismatches 11; Indels 6; Gaps 2;

QY 13 ROCMOLE-----TSGOMRRC-VSQCCKRFEEDIDMSKY 44
| | | | | : : : : : | | | | | : : : : : | | |
Db 104 rscdslnrcegsvqtrchigcdkrtkqdgyswh 141

RESULT 11
Y06183
ID Y06183 standard; Protein: 441 AA.
XX
AC Y06183;
XX
DT 16-AUG-1999 (first entry)
XX
DE Thrombospondin I fragment concatamer.
XX
KW Anti-angiogenic; carrier:DNA complex; tumour; gene therapy; human;
KW thrombospondin I; melanoma; lung cancer; colon cancer;
KW brain cancer; breast cancer; concatamer.
XX
OS Homo sapiens.
XX
XX
XX Key Location/Qualifiers
FH Misc-difference 33 /note= "encoded by GTT"
FT Misc-difference 34 /note= "encoded by GTT"
FT Misc-difference 81 /note= "encoded by GAT"
FT Misc-difference 81 /note= "encoded by GGC"
FT Misc-difference 82 /note= "encoded by TGC"
FT Misc-difference 97 /note= "encoded by AAT"
FT Misc-difference 98 /note= "encoded by GGA"
FT

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FT Misc-difference 160 /note= "encoded by CGG"
FT Misc-difference 383 /note= "encoded by CGG"
XX
XX EP921193-A1.
XX
XX 09-JUN-1999.
PD
XX
XX 07-JAN-1998; 98EP-0100135.
PF
XX 05-DEC-1997; 97US-0985526.
PR
XX
XX (MIXS/) MIXSON A J.
PA
XX
XX Mixson AJ;
PI
XX
XX WPI: 1999-315406/27.
DR N-PSDB: X58726.
XX
XX
PT Inhibition of growth of solid tumors
XX
XX
PS Disclosure: Page 19-20; 46pp; English.
XX
XX The present sequence represents a concatamer of anti-angiogenic fragments of thrombospondin I. The invention provides a carrier-DNA complex that comprises DNA (see X58725-42) encoding at least one anti-angiogenic protein or peptide, the complex being deliverable to the site of a tumour in vivo, and additionally comprises a regulatory elements for expressing the anti-angiogenic DNA in a tumour or tumour vasculature. The complex may also include DNA encoding a tumour suppressor protein, especially p53. The carrier is a liposome, cationic polymer, micelle, microsphere, virus, viral component, or a combination of these, and administration is by intravenous or intra-tumoral injection. The complexes are useful in gene therapy for inhibition of tumour growth. The types of tumors which may be treated include solid tumors such as melanomas and tumors in the lung, colon, brain and breast. Use of concatamers can increase the anti-angiogenic dosage level without altering the amount of vector necessary for delivery.

Sequence 441 AA;

```

Query Match 26.6%; Score 67; DB 20; Length 441;
Best Local Similarity 39.5%; Pred. NO. 1;
Matches 15; Conservative 6; Mismatches 11; Indels 6; Gaps 2.

QY 13 ROCMOLE-----TSGOMRRC-VSCCDKRFEEIDIDSKY 44
      | | | | | : | | | | | : | | | | | : | | |
Db 104 rscdslmncgsgsvqtrtchqgeckrkfkdgqgshw 141

RESULT 12
W90340
ID W90340 standard; protein; 444 AA.
XX
AC W90340;
XX
DT 24-MAY-1999 (first entry)
XX
DE G. max truncated SBP1 protein.
XX
DE SBP1; sucrose binding protein; SBP2; sucrose uptake; transgenic plant;
XX seed; carbohydrate content; soybean.
XX
XX Glycine max.
XX OS
XX PN WO9853086-A1.
XX PD
XX 26-NOV-1998.
XX
XX 21-MAY-1998; 98WO-US10465.
XX

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22-MAY-1997; 97US-0047568.
(UNIW) UNIV WASHINGTON STATE RES FOUND.
Chao WS, Grimes HD;
WPI: 1999-070155/06.
New modified plant sucrose binding proteins - used to develop transgenic plants which can have enhanced or decreased sucrose uptake activity in developing seeds
Claim 7; Page 36-37; 58pp; English.
This sequence represents a novel sucrose binding protein, SBP1 isolated from Glycine max. This protein is used in a method resulting in the production of a modified plant sucrose binding protein (SBP) which has a modified amino acid sequence compared to a corresponding wild-type SBP, and where expression of the modified SBP in a yeast assay system confers enhanced sucrose uptake compared to the corresponding wild-type SBP. The products of the invention can be used for producing transgenic plants which have modified sucrose uptake activity, particularly in developing seeds. Enhanced sucrose uptake activity in developing seeds may be desirable where it is an advantage to increase the carbohydrate content of the seed (e.g. where the seed is the primary plant material harvested, such as soybean). In contrast, decreased sucrose uptake activity in seeds might be desirable where the vegetative material of the plant is harvested. The SBP regulatory regions confer specific or enhanced expression in developing seeds and so may be used to express any transgene in developing seeds.

	Query Match	25.0%	Score 63	DB 20	Length 444
	Best Local Similarity	38.2%	Pred. No. 3.3		
	Matches	13	Conservative	4	Mismatches 15; Indels 2; Gaps 1;
Oy	2 EEDROYEECKRQCMOLE--TSGQMRRCVSQC DK	33			
db	34 eeedpelvtcknqcgqggytlegdkrvclgsdc	67			

RESULT	13
W90339	
ID	W90339 standard; protein; 524 AA.
XX	
AC	W90339;
XX	
DT	24-MAY-1999 (first entry)
XX	
DE	G. max SBP1 protein.
XX	
KW	SBP1; sucrose binding protein; SBP2; sucrose uptake; transgenic plant;
XX	
XX	seed; carbohydrate content; soybean.
XX	
OS	Glycine max.
XX	
PN	W09853086-A1.
XX	
PD	26-NOV-1998.
XX	
PF	21-MAY-1998; 98WO-US10465.
XX	
PR	22-MAY-1997; 97US-0047568.
XX	
PA	(UNIV) UNIV WASHINGTON STATE RES FOUND.
XX	
PI	Chao WS, Grimes HD;
XX	
DR	WPI; 1999-070155/06.
XX	

```

PT New modified plant sucrose binding proteins - used to develop
PT transgenic plants which can have enhanced or decreased sucrose
PT uptake activity in developing seeds
XX
XX Disclosure: Page 34-36; 58pp; English.
XX
XX This sequence represents a novel sucrose binding protein, SBP1 isolated
CC from Glycine max. This protein is used in a method resulting in the
CC production of a modified plant sucrose binding protein (SBP) which has a
CC modified amino acid sequence compared to a corresponding wild-type SBP,
CC and where expression of the modified SBP in a yeast assay system confers
CC enhanced sucrose uptake compared to the corresponding wild-type SBP.
CC The products of the invention can be used for producing transgenic plants
CC which have modified sucrose uptake activity, particularly in developing
CC seeds. Enhanced sucrose uptake activity in developing seeds may be
CC desirable where it is an advantage to increase the carbohydrate content
CC of the seed (e.g. where the seed is the primary plant material harvested,
CC such as soybean). In contrast, decreased sucrose uptake activity in
CC seeds might be desirable where the vegetative material of the plant is
CC harvested. The SBP regulatory regions confer specific or enhanced
CC expression in developing seeds and so may be used to express any
CC transgene in developing seeds.
XX
XX Sequence 524 AA:
SQ
XX
XX Query Match 25.0%; Score 63; DB 20; Length 524;
XX Best Local Similarity 38.2%; Pred. NO. 3.9;
XX Matches 13; Conservative 4; Mismatches 15; Indels 2; Gaps 1
Oy 2 EPDRQYEERCKRQCMQLE--TSQMRCYSQCDK 33
Oy | : | | | | | : | : | | | : | | :
Db 34 eeedpelvtckhqcgqgqylegdkrvclqscdr 67

RESULT 14
M90342
XX W90342 standard; protein; 409 AA.
XX
XX W90342:
XX
XX 24-MAY-1999 (first entry)
XX
XX G. max truncated SBP2 protein.
XX
XX SBP1: sucrose binding protein; SBP2: sucrose uptake; transgenic plant;
KW seed; carbohydrate content; soybean.
XX
XX Glycine max.
OS
XX W09853086-A1.
XX
XX 26-NOV-1998.
XX
XX 21-MAY-1998; 98WO-US10465.
XX
XX 22-MAY-1997; 97US-0047568.
XX
XX (UNIM ) UNIV WASHINGTON STATE RES FOUND.
XX
XX Chao WS, Grimes HD;
XX
XX WPI: 1999-070155/06.
XX
XX New modified plant sucrose binding proteins - used to develop
PT transgenic plants which can have enhanced or decreased sucrose
PT uptake activity in developing seeds
XX
XX Claim 7; Page 39-40; 58pp; English.
XX
XX This sequence represents a novel sucrose binding protein, SBP2 isolated
CC from Glycine max. This protein is used in a method resulting in the
CC production of a modified plant sucrose binding protein (SBP) which has a
CC production of a modified plant sucrose binding protein (SBP) which has a

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CC	modified amino acid sequence compared to a corresponding wild-type SBP,
CC	and where expression of the modified SBP in a yeast assay system confers
CC	enhanced sucrose uptake compared to the corresponding wild-type SBP.
CC	The products of the invention can be used for producing transgenic plants
CC	which have modified sucrose uptake activity, particularly in developing
CC	seeds. Enhanced sucrose uptake activity in developing seeds may be
CC	desirable where it is an advantage to increase the carbohydrate content
CC	of the seed (e.g. where the seed is the primary plant material harvested,
CC	such as soybean). In contrast, decreased sucrose uptake activity in
CC	seeds might be desirable where the vegetative material of the plant is
CC	harvested. The SBP regulatory regions confer specific or enhanced
CC	expression in developing seeds and so may be used to express any
CC	transgene in developing seeds.
SQ	
XX	Sequence 409 AA;
XX	
XX	
XX	Query Match 24.8%; Score 62.5; DB 20; Length 409;
XX	Best local Similarity 36.6%; Pred. NO. 3.5;
XX	Matches 15; Conservative 3; Mismatches 14; Indels 9; Gaps 2;
OY	
Db	7 EYECKRQCQMLE--TSGMRRCVSQCD-----KRFEPD 38 38 elvtckhgqgqrgrfyesdkrtclqgcsmkqerekvsee 78
RESULT 15	
ID W90341	W90341 standard; protein; 489 AA.
AC W90341:	
XX	
XX	24-MAY-1999 (first entry)
DE	G. max SBP2 protein.
XX	
KW	SBP1; sucrose binding protein; SBP2; sucrose uptake; transgenic plant; seed; carbohydrate content; soybean.
OS	Glycine max.
PN MO9853086-A1.	
PD 26-NOV-1998.	
PF 21-MAY-1998;	98WO-US10465.
PR 22-MAY-1997;	97US-0047568.
PA (UNITV) UNIV WASHINGTON STATE RES FOUND.	
PI Chao WS, Grimes HD;	
DR WPI: 1999-070155/06.	
PT New modified plant sucrose binding proteins - used to develop	
PT transgenic plants which can have enhanced or decreased sucrose	
PT uptake activity in developing seeds	
PS Claim 13b; Page 37-38; 58pp; English.	
XX	
XX	This sequence represents a novel sucrose binding protein, SBP2 isolated
CC from glycine max. This protein is used in a method resulting in the	
CC production of a modified plant sucrose binding protein (SBP) which has a	
CC modified amino acid sequence compared to a corresponding wild-type SBP,	
CC and where expression of the modified SBP in a yeast assay system confers	
CC enhanced sucrose uptake compared to the corresponding wild-type SBP.	
CC The products of the invention can be used for producing transgenic plants	
CC which have modified sucrose uptake activity, particularly in developing	
CC seeds. Enhanced sucrose uptake activity in developing seeds may be	
CC desirable where it is an advantage to increase the carbohydrate content	
CC of the seed (e.g. where the seed is the primary plant material harvested,	
CC such as soybean). In contrast, decreased sucrose uptake activity in	

